

SEQUENCE LISTING

<110> Presnell, Scott R.
 Xu, Wenfeng
 Kindsvogel, Wayne
 Chen, Zhi

<120> Mouse Cytokine Receptor

<130> 01-08

<150> US 60/273,035

<151> 2001-03-02

<150> US 60/279,232

<151> 2001-03-27

<160> 49

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(693)

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atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt	48
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu	
1 5 10 15	

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag	96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln	
20 25 30	

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag	144
---	-----

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
35 40 45	
cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac	192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
50 55 60	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	

gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa 672
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

gag aga tgt gtg gaa att cca tgacttggtg aatttggtat tcagcaatgt 723
 Glu Arg Cys Val Glu Ile Pro
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tatttaaaat 783
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843
 ccattctttt atcctttata tttcatttta aactatattt gaacgacatt ccccccgaag 903
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aacttttattt 963
 ctgaatgtaa catccctaata aacaaccttc attcttctaa tacagcaaaa taaaaattta 1023
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 tgttttaaag tctactttat gtaaataaga acagggtttt gggaaaaaaa tcttatgatt 1323
 tctggattga tatctgaatt aaaactatca acaacaagga agtctactct gtacaattgt 1383
 ccctcattta aaagatatat taagcttttc ttttctgttt gtttttgttt tgtttagttt 1443
 ttaatcctgt cttagaagaa cttatcttta ttctcaaaat taaatgtaat ttttttagtg 1503
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 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgtctt 1863
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagtg ataaatggat 1983
 taaaaaatat tcagaaatgt attggggggg ggaggagaat aagaggcaga gcaagagcta 2043
 gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103
 gagactgaaa aaaaaaaaaa gctcgagcgg ccgccatata cttggt 2149

<210> 2

<211> 231

<212> PRT

<213> Homo sapiens

<400> 2

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220
 Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 3

<211> 693

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the
amino acid sequence of SEQ ID NO:2

<221> misc_feature

<222> (1)...(693)

<223> n = A,T,C or G

<400> 3

atgatgccna arcaytgytt yytnggntty ytnathwsnt tyttyytnac nggngtngcn 60
 ggnacncarw snacncayga rwsnytnaar ccncarmng tncarttyca rwsnmgnaay 120

ttycayaaya	thytncartg	gcarccnggn	mgngcnytna	cnggnaayws	nwsngtntay	180
ttygtncart	ayaarathta	yggncarmgn	cartggaara	ayaargarga	ytgytggggn	240
acncargary	tnwsntgyga	yytnacnwsn	garacnwsng	ayathcarga	rccntaytay	300
ggnmgngtnm	gngcngcnws	ngcnggnwsn	taywsngart	ggwsnatgac	nccnmgnnty	360
acnccntggt	gggaracnaa	rathgayccn	ccngtnatga	ayathacnca	rgtnaayggn	420
wsnytnytn	tnathytnca	ygcncnaay	ytncntaym	gntaycaraa	rgaraaraay	480
gtnwsnathg	argaytayta	ygarytnytn	taymgngtnt	tyathathaa	yaaywsnytn	540
garaargarc	araargnta	ygargngcn	caymgngcng	tngarathga	rgcnytnacn	600
ccncaywsnw	sntaytgygt	ngtngcngar	athtaycarc	cnatgytnga	ymgnmgngwsn	660
carmgnwsng	argarmgntg	ygtngarath	ccn			693

<210> 4

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

<400> 4

Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
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<210> 5

<211> 699

<212> DNA

<213> Homo sapiens

<400> 5

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ggggcaccgt	cagtcttcct	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	120
acccttgagg	tcacatgctg	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcttccat	cgagaaaacc	360
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	420
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacgcaga	agagcctctc	cctgtctccg	ggtaaataa			699

<210> 6

<211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC29181

<400> 6
 gcggatccac tcagtcaacg catgagtctc tg 32

<210> 7
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC29182

<400> 7
 gcagatcttg gaatttcac acatctctct tca 33

<210> 8
 <211> 108
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(108)

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 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc 96
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30

ttc cgt aga tcc 108
 Phe Arg Arg Ser
 35

<210> 9
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30
 Phe Arg Arg Ser
 35

<210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Glu-Glu (CEE) Tag amino acid sequence

<400> 10
 Glu Tyr Met Pro Met Glu
 1 5

<210> 11
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG Tag amino acid sequence

<400> 11
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 12
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> His Tag amino acid sequence

<400> 12

His His His His His His

1

5

<210> 13

<211> 210

<212> PRT

<213> Homo sapiens

<400> 13

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		20					25						30		
Thr	Gly	Asn	Ser	Ser	Val	Tyr	Phe	Val	Gln	Tyr	Lys	Ile	Tyr	Gly	Gln
	35						40					45			
Arg	Gln	Trp	Lys	Asn	Lys	Glu	Asp	Cys	Trp	Gly	Thr	Gln	Glu	Leu	Ser
	50				55					60					
Cys	Asp	Leu	Thr	Ser	Glu	Thr	Ser	Asp	Ile	Gln	Glu	Pro	Tyr	Tyr	Gly
65				70					75					80	
Arg	Val	Arg	Ala	Ala	Ser	Ala	Gly	Ser	Tyr	Ser	Glu	Trp	Ser	Met	Thr
			85					90						95	
Pro	Arg	Phe	Thr	Pro	Trp	Trp	Glu	Thr	Lys	Ile	Asp	Pro	Pro	Val	Met
			100					105						110	
Asn	Ile	Thr	Gln	Val	Asn	Gly	Ser	Leu	Leu	Val	Ile	Leu	His	Ala	Pro
	115					120						125			
Asn	Leu	Pro	Tyr	Arg	Tyr	Gln	Lys	Glu	Lys	Asn	Val	Ser	Ile	Glu	Asp
	130					135					140				
Tyr	Tyr	Glu	Leu	Leu	Tyr	Arg	Val	Phe	Ile	Ile	Asn	Asn	Ser	Leu	Glu
145				150						155				160	
Lys	Glu	Gln	Lys	Val	Tyr	Glu	Gly	Ala	His	Arg	Ala	Val	Glu	Ile	Glu
			165					170						175	
Ala	Leu	Thr	Pro	His	Ser	Ser	Tyr	Cys	Val	Val	Ala	Glu	Ile	Tyr	Gln
			180					185					190		
Pro	Met	Leu	Asp	Arg	Arg	Ser	Gln	Arg	Ser	Glu	Glu	Arg	Cys	Val	Glu
	195					200						205			
Ile	Pro														
	210														

<210> 14

<211> 1116
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (21)...(557)

<400> 14

tcgagtaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc 53
 Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe
 1 5 10

ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg 101
 Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
 15 20 25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac 149
 Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
 30 35 40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg 197
 Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
 45 50 55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245
 Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
 60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
 Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
 80 85 90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341
 Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
 95 100 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
 Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
 110 115 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu

125

130

135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
 140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
 160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
 Met Ser Leu Arg Asn Ala Cys Ile
 175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
 aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
 tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag acttttctaag 767
 catagatatt tattgataac atttcattgt aactgggtgt ctatacacag aaaacaattt 827
 attttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
 aaacccttaa atagcttcat gtttccataa tcagtacttt atattttataa atgtatttat 947
 tattattata agactgcatt ttattttatat cattttatta atatggattt atttatagaa 1007
 acatcattcg atattgctac ttgagtgtaa ggctaataat gatatttatg acaataatta 1067
 tagagctata acatgtttat ttgacctcaa taaacacttg gatataccta 1116

<210> 15

<211> 179

<212> PRT

<213> Homo sapiens

<400> 15

Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
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 Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln

100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 16
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC25963

<400> 16
 agtcaacgca tgagtctctg aag

23

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC28354

<400> 17
 accaacaag agccattgac ttg

23

<210> 18
 <211> 23
 <212> DNA
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<220>
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<400> 18

gaggagacca taacccccga cag

23

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21196

<400> 19

catagctccc accacacgat ttt

23

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC14063

<400> 20

caccagacat aatagctgac agact

25

<210> 21

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC17574

<400> 21

ggtrttgctc agcatgcaca c

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<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC17600

<400> 22

catgtaggcc atgaggtcca ccac

24

<210> 23

<211> 22

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Oligonucleotide primer ZC27659

<400> 23

tcaagctgag ttctctgtat gg

22

<210> 24

<211> 2831

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (34)...(1755)

<400> 24

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Met Arg Thr Leu Leu Thr Ile

1

5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat 102

Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp

10

15

20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150

Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

25

30

35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198

Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile

40

45

50

55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246

Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys

60

65

70

cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn 75 80 85	294
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly 90 95 100	342
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr 105 110 115	390
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile 120 125 130 135	438
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly 140 145 150	486
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu 155 160 165	534
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln 170 175 180	582
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly 185 190 195	630
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr 200 205 210 215	678
atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe 220 225 230	726
tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	774

235	240	245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser 250 255 260			822
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln 265 270 275			870
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu 280 285 290 295			918
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu 300 305 310			966
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu 315 320 325			1014
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cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val 345 350 355			1110
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro 360 365 370 375			1158
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala 380 385 390			1206
cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met 395 400 405			1254
gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa			1302

Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	
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cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc	1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
425	430 435
tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg	1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
440	445 450 455
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc	1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
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aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg	1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
475	480 485
aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag	1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	
490	495 500
atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca	1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
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tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc	1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
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ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca	1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	
540	545 550
gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc	1734
Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala	
555	560 565
ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tggtgcttcc	1785
Leu Thr Val Gln Trp Glu Ser	
570	


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<211> 574

<212> PRT

<213> Homo sapiens

<400> 25

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Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35             40             45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50             55             60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65             70             75             80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85             90             95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
100            105            110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
115            120            125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
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Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
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 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
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 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
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 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
 225 230 235 240
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
 245 250 255
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
 260 265 270
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
 275 280 285
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
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 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
 305 310 315 320
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
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 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
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 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
 355 360 365
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
 370 375 380
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
 385 390 395 400
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
 405 410 415
 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
 420 425 430
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu

	485		490		495										
Pro	Leu	Leu	Ser	Ser	Val	Gln	Ile	Glu	Gly	His	Pro	Met	Ser	Leu	Pro
	500							505					510		
Leu	Gln	Pro	Pro	Ser	Gly	Pro	Cys	Ser	Pro	Ser	Asp	Gln	Gly	Pro	Ser
	515						520					525			
Pro	Trp	Gly	Leu	Leu	Glu	Ser	Leu	Val	Cys	Pro	Lys	Asp	Glu	Ala	Lys
	530					535				540					
Ser	Pro	Ala	Pro	Glu	Thr	Ser	Asp	Leu	Glu	Gln	Pro	Thr	Glu	Leu	Asp
545				550					555					560	
Ser	Leu	Phe	Arg	Gly	Leu	Ala	Leu	Thr	Val	Gln	Trp	Glu	Ser		
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<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide linker ZC13252

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<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC25963

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23

<210> 31

<211> 23

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<213> Artificial Sequence

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<223> Oligonucleotide primer ZC25964

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<210> 32

<211> 18

<212> DNA

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<223> Oligonucleotide primer ZC14666

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18

<210> 33

<211> 22

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<211> 211

<212> PRT

<213> Homo sapiens

<400> 34

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Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp	35	40	45	
Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	50	55	60	
Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	65	70	75	80
Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	85	90	95	
Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	100	105	110	
Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	115	120	125	
Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	130	135	140	
Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	145	150	155	160
His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	165	170	175	
Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala				

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 195 200 205
 Thr Trp Thr
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<210> 35
 <211> 199
 <212> PRT
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 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
 180 185 190
 Thr Thr His Asp Glu Thr Val
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<210> 36
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 36

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 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
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 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
 195 200 205
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<210> 37

<211> 2464

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (8)...(697)

<400> 37

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ttg agc agt gca aca gaa ata caa cca gct cgt gta tct ctg acg ctc			97
Leu Ser Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Leu			
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cag aag gtc cga ttt cag tcc aga aat ttc cac aat att ttg cac tgg			145
Gln Lys Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp			
	35	40	45
caa gca ggg agc tct ctc ccc agc aac aac agc atc tac ttt gtg cag			193
Gln Ala Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln			
	50	55	60
tac aag atg tat gga cag agc caa tgg gaa gat aaa gtt gac tgc tgg			241
Tyr Lys Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp			
	65	70	75
ggg acc acg gcg ctc ttc tgt gac ctg acc aat gaa acc tta gac cca			289
Gly Thr Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro			
	80	85	90
tac gag ctg tat tac ggg agg gtg atg acg gcc tgt gct gga cgc cac			337
Tyr Glu Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His			
	95	100	105
tct gcc tgg acc agg aca ccc cgc ttc act cca tgg tgg gaa aca aaa			385
Ser Ala Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys			
	115	120	125
cta gat cct ccg gtc gtg act ata acc cga gtt aac gca tct ttg cgg			433
Leu Asp Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg			
	130	135	140
gtg ctt ctc cgt cct cca gag ttg cca aat aga aac caa agt gga aaa			481
Val Leu Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys			
	145	150	155
aat gca tcc atg gaa act tac tac ggc tta gta tac aga gtt ttc aca			529
Asn Ala Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr			
	160	165	170
atc aac aat tca cta gag aag gag caa aaa gcc tat gaa gga act cag			577

Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln
175 180 185 190

aga gct gtt gaa att gaa ggt ctg ata cct cat tcc agc tac tgc gta 625
Arg Ala Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val
195 200 205

gtg gct gaa atg tac cag ccc atg ttt gac aga aga agc cca aga agc 673
Val Ala Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser
210 215 220

aag gag aga tgt gtg cag att cca tgaactggctc tgaggcgcta aaaccggaag 727
Lys Glu Arg Cys Val Gln Ile Pro
225 230

catattgaga acaggatgtc ttctgcctag aacagcttac taaacttctg ttttgatttt 787
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2464

<210> 38

<211> 230

<212> PRT

<213> Mus musculus

<400> 38

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 Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala
 35 40 45
 Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys
 50 55 60
 Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr
 65 70 75 80
 Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu
 85 90 95
 Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala
 100 105 110
 Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp
 115 120 125
 Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu
 130 135 140
 Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala
 145 150 155 160
 Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn
 165 170 175
 Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala
 180 185 190
 Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala
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 Arg Cys Val Gln Ile Pro
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<210> 39

<211> 690

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of SEQ ID NO:38

<221> misc_feature

<222> (1)...(690)

<223> n = A,T,C or G

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cayaayathy tncaytggca rgcnggnwsn wsnytnccnw snaayaayws nathtaytty	180
gtncartaya aratgtaygg ncarwsncar tgggargaya argtngaytg ytggggnacn	240
acngcnytn tytgygayt nacnaaygar acnytngayc cntaygaryt ntaytaygg	300
mgngtnatga cngcntgygc nggmngncay wsngcntgga cnmgnacncc nmngnttyacn	360
ccntggtggg aracnaaryt ngayccnccn gtngtnacna thacnmngnt naaygcwnsn	420
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wsnatggara cntaytaygg nytngtntay mgngtnttya cnathaayaa ywsnytnгар	540
aargarcara argcntayga rggnacncar mgngcngtnг arathgargg nytnathccn	600
caywsnwsnt aytgygtngt ngcngaratg taycarccna tgattygaymg nmgnwsnccn	660
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<210> 40

<211> 1050

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (50)...(589)

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Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala Ala Ser	
5 10 15	
tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat gcg ctg ccc	154
Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala Leu Pro	
20 25 30 35	

atc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag cag ccg tac 202
 Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln Pro Tyr
 40 45 50

atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc ctt gca gat 250
 Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu Ala Asp
 55 60 65

aac aac aca gac gtc cgg ctc atc ggg gag aaa ctg ttc cga gga gtc 298
 Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg Gly Val
 70 75 80

agt gct aag gat cag tgc tac ctg atg aag cag gtg ctc aac ttc acc 346
 Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn Phe Thr
 85 90 95

ctg gaa gac att ctg ctc ccc cag tca gac agg ttc cgg ccc tac atg 394
 Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg Pro Tyr Met
 100 105 110 115

cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag ctc agc tcc 442
 Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu Ser Ser
 120 125 130

tgt cac atc agt ggt gac gac cag aac atc cag aag aat gtc aga agg 490
 Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val Arg Arg
 135 140 145

ctg aag gag aca gtg aaa aag ctt gga gag agc gga gag atc aaa gcg 538
 Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala
 150 155 160

atc ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat gct tgc gtc 586
 Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Val
 165 170 175

tga gcgagaagaa gctagaaaac gaagaactgc tccttcctgc cttctaaaaa 639
 *

gaacaataag atccctgaat ggactttttt actaaaggaa agtgagaagc taacgtccac 699
 catcattaga agatttcaca tgaaacctgg ctcagttgaa agagaaaata gtgtcaagtt 759

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gtccatgaga ccagaggtag acttgataac cacaaagatt cattgacaat attttattgt      819
cattgataat gcaacagaaa aagtatgtac tttaaaaaat tgtttgaaag gaggttacct      879
ctcattcctc tagaagaaaa gcctatgtaa cttcatttcc ataaccaata ctttatatat      939
gtaagtttat ttattataag tatacatttt atttatgtca gtttattaat atggatttat      999
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<210> 41

<211> 179

<212> PRT

<213> Mus musculus

<400> 41

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Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
      20              25              30
Ala Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
      35              40              45
Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
      50              55              60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
      65              70              75              80
Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
      85              90              95
Asn Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg
      100             105             110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
      115             120             125
Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
      130             135             140
Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
      145             150             155             160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
      165             170             175
Ala Cys Val

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<210> 42

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC10651

<400> 42

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20

<210> 43

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC10565

<400> 43

tttgcagaaa aggttgcaaa tgc

23

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC38001

<400> 44

ccgttcgtga ctataacccg

20

<210> 45

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38022

<400> 45

agccgtagta agtttccat

19

<210> 46

<211> 4

<212> PRT

<213> Artificial Sequence

<223> SXWS polypeptide motif

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<223> Xaa = Any Amino Acid

Ser Xaa Trp Ser

1

<211> 707

<213> Mus musculus

<221> CDS

<222> (2) ... (691)

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Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu Ser
1 5 10 15

agt gca aca gaa ata caa cca gct cgt gta tct ctg acg ccc cag aag 97
Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Pro Gln Lys
20 25 30

gtc cga ttt cag tcc aga aat ttc cac aat att ttg cac tgg caa gca 145
Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala
35 40 45

ggg agc tct ctc ccc agc aac aac agc atc tac ttt gtg cag tac aag 193
Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys
50 55 60

atg tat gga cag agc caa tgg gaa gat aaa gtt gac tgc tgg ggg acc 241
Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr
65 70 75 80

acg gcg ctc ttc tgt gac ctg acc aat gaa acc tta gac cca tac gag 289
Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu

	85	90	95	
ctg tat tac ggg agg gtg atg acg gcc tgt gct gga cgc cac tct gcc				337
Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala				
	100	105	110	
tggt acc agg aca ccc cgc ttc act cca tgg tgg gaa aca aaa cta gat				385
Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp				
	115	120	125	
cct ccg gtc gtg act ata acc cga gtt aac gca tct ttg cgg gtg ctt				433
Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu				
	130	135	140	
ctc cgt cct cca gag ttg cca aat aga aac caa agt gga aaa aat gca				481
Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala				
	145	150	155	160
tcc atg gaa act tac tac ggc tta gta tac aga gtt ttc aca atc aac				529
Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn				
	165	170	175	
aat tca cta gag aag gag caa aaa gcc tat gaa gga act cag aga gct				577
Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala				
	180	185	190	
gtt gaa att gaa ggt ctg ata cct cat tcc agc tac tgc gta gtg gct				625
Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala				
	195	200	205	
gaa atg tac cag ccc atg ttt gac aga aga agc cca aga agc aag gag				673
Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu				
	210	215	220	
aga tgt gtg cac att cca tgaactgggtc tgaggc				707
Arg Cys Val His Ile Pro				
	225	230		

<210> 48

<211> 230

<212> PRT

<213> Mus musculus

<400> 48

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Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu Ser
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Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Pro Gln Lys
          20          25          30
Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala
          35          40          45
Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys
          50          55          60
Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr
65          70          75          80
Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu
          85          90          95
Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala
          100          105          110
Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp
          115          120          125
Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu
          130          135          140
Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala
145          150          155          160
Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn
          165          170          175
Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala
          180          185          190
Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala
          195          200          205
Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu
          210          215          220
Arg Cys Val His Ile Pro
225          230

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<210> 49

<211> 690

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of SEQ ID NO:48

<221> misc_feature

<222> (1)...(690)

<400> 49

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athcarccng	cnmgngtnws	nytnacncn	caraargtnm	gnattyarws	nmgnaaytty	120
cayaayathy	tncaytggca	rgcnggnwsn	wsnytnccnw	snaayaayws	nathtaytty	180
gtncartaya	aratgtaygg	ncarwsncar	tgggargaya	argtngaytg	ytggggnacn	240
acngcnytn	tytgygayyt	nacnaaygar	acnytngayc	cntaygaryt	ntaytayggn	300
mgngtnatga	cngcntgygc	nggnmgncay	wsngcntgga	cnmgnacncc	nmgnattyacn	360
ccttggtggg	aracnaaryt	ngayccncn	gtngtnacna	thacnmngnt	naaygcwnsn	420
ytnmgngtny	tnytnmgnc	ncngarytn	ccnaaymgna	aycarwsngg	naaraaygcn	480
wsnatggara	cntaytaygg	nytngtntay	mgngtnatty	cnathaayaa	ywsnytngar	540
aargarcara	argcntayga	rggnacncar	mgngcngtn	arathgargg	nytnathccn	600
caywsnwsnt	aytgygtngt	ngcngaratg	taycarccna	tgtygayymg	nmgnwsnccn	660
mgnwsnaarg	armgntgygt	ncayathccn				690